

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 14, 2003, 09:23:54 ; Search time 19.4774 Seconds
(without alignments)
3287.177 Million cell updates/sec

Title: US-09-836-077-3

Perfect score: 3615

Sequence: 1 MTPPPGRAPASAPRARVPG.....LAASLMLGLPTLTLGLLVH 666

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_73:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	37.4	653	2 T03102	semaphorin homolog
2	654.5	18.1	771	2 D49423	semaphorin III pre
3	632.5	17.5	772	2 A49069	collapsin - chick
4	628.5	17.4	748	2 I48744	semaphorin A - mou
5	621	17.2	772	2 I48747	semaphorin D - mou
6	617	17.1	749	2 G01856	semaphorin V - hum
7	617	17.1	782	2 I48746	semaphorin C - mou
8	612	16.9	666	2 I58169	semaphorin III - m
9	611	16.9	753	2 G02173	semaphorin III fam
10	597.5	16.5	751	2 I48748	semaphorin E - mou
11	485.5	13.4	760	2 I48745	semaphorin B - mou
12	479.5	13.3	834	2 S66498	M-sema F protein p
13	452	12.5	730	2 JH0798	fasciclin IV precu
14	411	11.4	712	2 T27165	hypothetical prote
15	409	11.3	1074	2 JC5928	semaphorin F precu
16	408.5	11.3	711	2 A49423	semaphorin I precu
17	407	11.3	724	2 C49423	semaphorin II precu
18	399	11.0	656	2 B49423	semaphorin I - fru
19	364	10.1	441	2 S29921	hypothetical prote
20	363	10.0	403	2 E42521	A39r protein - vac
21	312	8.6	676	2 T33853	hypothetical prote
22	236.5	6.5	2051	2 T13164	plexin B - fruit f
23	228	6.3	295	2 JQ1775	Salp19r protein - v
24	215	5.9	1894	2 JC4980	plexin 1 precursor
25	190	5.3	1945	2 T13937	plexin A - fruit f
26	186	5.1	1905	2 I51553	plexin - African c
27	174	4.8	1872	2 JC4976	plexin 3 precursor
28	170	4.7	1884	2 JC4975	plexin 2 precursor
29	139	3.8	1375	1 JC5148	hepatocyte growth

30	133	3.7	1425	2 T30811	hepatocyte growth
31	129	3.6	1568	2 T09074	semaphorin recepto
32	124.5	3.4	620	2 T30765	hypothetical prote
33	122	3.4	1404	1 A48196	protein-tyrosine k
34	114	3.2	142	2 JQ1776	Salp1r protein - v
35	113.5	3.1	1376	2 G00043	osteonidogen - hum
36	113.5	3.1	1658	2 D86890	DNA-directed DNA p
37	112.5	3.1	1302	2 B41249	multidrug resistan
38	111	3.1	122	2 C72169	A46r protein - var
39	111	3.1	122	2 H36852	A43r protein - var
40	111	3.1	122	2 T28584	14r protein - var
41	109.5	3.0	1379	1 S01254	hepatocyte growth
42	106.5	2.9	637	2 JQ2039	polyprotein - pars
43	106.5	2.9	1792	2 T08878	supervillin p205 -
44	105.5	2.9	622	2 S62580	probable multicopp
45	105.5	2.9	1271	2 T43269	microcystin synthe

ALIGNMENTS

RESULT 1

T03102 semaphorin homolog A3 - alcelaphine herpesvirus 1

C:Species: alcelaphine herpesvirus 1

C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #ext_change 08-Oct-1999

C:Accession: T03102

R:Enser, A.; Pfeizer, R.; Fleckenstein, B.

J. Virol. 71, 6517-6525, 1997

A:Title: Primary structure of the alcelaphine herpesvirus 1 genome.

A:Reference number: Z14840; M0ID:97404659; PMID:9261371

A:Accession: T03102

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-653 <ENS>

A:Cross-References: EMBL:AF005370; NID:92337967; PIDN:AAC58054.1; PID:92337970

Query Match 37.4%; Score 1353; DB 2; Length 653;

Best Local Similarity 45.9%; Pred. No. 1.7e-95;

Matches 277; Conservative 86; Mismatches 228; Indels 12; Gaps 7;

QY	22	PARLG-LPLRLRLLLMAAASAGHLRSGRIFAVWKGHGQDRVDEGOTEPHTVLFH 80	
DB	45	PAAMGTLGVISIRLMLT-SAITAAKSREIFDKPRLIVLFDGFGQHRF-FGQRPHTVLFH 102	
QY	81	EPSSSVWVGCRKGVYLFDPBEKNASVRYVNGSRKSGOLDKRRDCENTTLERSEGL 140	
DB	103	SLNSTDVYVGNNFTYLFDFAHSSNASTALINTSTHNRHSSTCENFTLLHNOTDGL 162	
QY	141	LACGTNARHPSCWNLVNGTVPLGEMRGYAPFSPDENSLVLPFGDEYVSTIRKQENGI 200	
DB	163	LACGTNSOKRSCWNLVNGTVPLGEMRGYAPFSPDENSLVLPFGDEYVSTIRKQENGI 222	
QY	201	PRFRIRGESELYSDPTWONPOFIKATVHDOADYDKTYFFREDNDPKNEADPLNV 260	
DB	223	HKFRRIAGVELYSDPTWONPOFIKATVHDOADYDKTYFFREDNDPKNEADPLNV 282	
QY	261	RVALOGRGOOGGESSLSVSKWNTFLKAMLYCSAATTKNNRLODVFLRDPDGGOMDTR 320	
DB	283	RVALOGRGOOGGESSLSVSKWNTFLKAMLYCSAATTKNNRLODVFLRDPDGGOMDTR 342	
QY	321	VYGVFSNPMNYSACVYSLDIDKVFRTSLKGYHSSLPNRPQKCLPDQOPIPTETFOV 380	
DB	343	YIGLFLSPNMFSAVCFTYVDIDHVFRTSLKGYHSSLPNRPQKCLPDQOPIPTETFOV 402	
QY	381	ADRHPEVAQDEVDMPGLKPLPLFSKYHYOKVAVHMQASGEPF--HVLVLTGDRGTIRK 438	
DB	403	ADRYPEVAQDEVDMPGLKPLPLFSKYHYOKVAVHMQASGEPF--HVLVLTGDRGTIRK 460	
QY	439	VYVPGDEHSEFARNIMEIQFRRAALQMSLDAERKLLVYSSQMEVSPQPLDCEYGG 498	
DB	461	YVAREDSNSTTALTEINEFQRPAPLQNTLNDNTNKLTVNSEVSEVPLDCLSVYGN 520	

OY 499 GCHGCLMSRDPYCGMDGRCISYSSERSVYLOSINPAEP--HKECPNPKDAPLQKVS 556
 DB 521 DCFSCMSRDPPLCTWYNNMC---SFKQVSVETGSGPANRTLSMCGHVAPTVKKQVSI 577
 OY 557 APSRYYLSCPMESRHATYSMRHKEVQSCFEGHOSPCNLTLENTLAQVGHYCEAQ 616
 DB 578 PLLSNSTYLSCPAVSNADYFWTKDGTETKCHVKTIKNDICILTAUSTATNGTHVCNMK 637
 OY 617 EGS 619
 DB 638 EDS 640

RESULT 2

D49423
 semaphorin III precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
 C:Accession: D49423
 R:Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
 Cell 75, 1389-1399, 1993
 A:Title: The semaphorin genes encode a family of transmembrane and secreted growth cone
 A:Reference number: A49423; MUID:94094332; PMID:8269517
 A:Session: D49423
 A:Status: preliminary; nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-771 <COL>
 A:Cross-references: GB:L26081; NID:9799328; PIDN:AAA65938.1; PID:9436560
 C:Genetics:
 A:Gene: GDB:SEMA1
 A:Cross-references: GDB:283448
 C:Superfamily: semaphorin

Query Match 18.1%; Score 654.5; DB 2; Length 771;
 Best Local Similarity 28.2%; Pred. No. 6.9e-42;
 Matches 194; Conservative 115; Mismatches 280; Indels 99; Gaps 27;

OY 32 RLILLMAAASQGLRSG---PRIFAVMKGVGDVND-----FGQTEPHTVLFHER 82
 DB 6 RIVCLFVGVLTLARANYQNGKNNPRLKLSYKEMESNNVTFPGLANGSSYHTFLDEE 65
 OY 83 GSSVWVGGRGVYLFDFPEGRKNASVTVNIGSTR-----GSCLDKRCENYITLLER 135
 DB 66 -RSRLVYGKDHIFSPDLVNIKDFQIVPVYSTRDECKMAGKDLK-ECANFIVLKA 123
 OY 136 RSE-GLACGTNARHPSCMNLVNGVVLGEM-----RGYAPFSPDENS 178
 DB 124 YNQTLLYACGTGAFHPC-----TYIEIGHREDNIFKLENSHPENGGRKSPYDKLLT 177
 OY 179 LVLFEGDEVYSTRKQEVNGKIPRRFRIGSELYT---SDTVMONPOFIKATVHQ-DQ 234
 DB 178 ASLLIDGELYSGTAADFMGRDFAIFRTLGHHPIRTDQHSRWLNDPKFISAHLSIESDN 237
 OY 235 AYDDKIYFFREDNPDKNPEAPLVNSRYAQLCRGDGESSLSVKNWFLAAMLUCSDA 294
 DB 238 PEDDKVYFFERNALIDGELSGKATHARIQICKNDPFGHRL-VNKKWTFLLARLICSP 296
 OY 295 ATN---KNFNRLQDVFL--PDPSGQMDTRVYGVF---SNPMWYSAVCVSLGIDKYF 346
 DB 297 GNGIDTHTDELQVFLMFKDP---KNPVYGVFTTSSNIFKSGAVCMYSMDVRYVF 352
 OY 347 -----RTSSLKGYHSLPNRPGKC-----LPDQOQIPIETFPVADRHREVAOR 390
 DB 353 LGPVYAHGDPNRYQWVYOGGRVYPRPGTCKPSTFGGFDSTKDLDPDVITFAARSHPMYNP 412
 OY 391 VEPMG-----PLKPLFHSKYHYQAVVHMAQSHGETFVLLTLTDRGTIHKVVE-PCGQ 445
 DB 413 VEPMMNRPLVITDY---NYQFTQIVDVRVDAEDGQ-YDVMEIGDVGIVLKVVSIPKFT 468
 OY 446 EHSFAFNIM-ETQPPRRAALQIOTMSLDAERKRLVYSSQWESQVPLDLCEVYGGGCHGL 504
 DB 469 WYDLEEVLEEMTVREPTVATISAMELSTKQOOLYIGSTAGVADQLPDLHRDDIIGKACABCC 528

OY 505 MSRDPYCGMDGRCISY--SSERSVYLOSINPAEPHKECPNPKDCK---APLQKVS-A 557
 DB 529 LADPVCAMGDSACSRYEPTAKRRTRQDIRNDPDLTHCSDDLHNDHNGHSPERIYGV 588
 OY 558 PNRYYLSCMESRHATYSMRHKEVQSCFEGHOSPCNLTLENTLAQVGHYCEAQ 612
 DB 589 ENSSTFLECSKQSRALVYQFQRRNEERKEEIRVDHIIIRTDGILLRSLQKSGNLY 648
 OY 613 CEAGESYFREAOHQMLLPEDGIMAEHL 640
 DB 649 CHAVEHGFQTLKVTL---EVIDTEHL 673

RESULT 3

A49069
 collapsin - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
 C:Accession: A49069
 R: Luo, Y.; Raible, D.; Raper, J.A.
 Cell 75, 217-227, 1993
 A:Title: Collapsin: a protein in brain that induces the collapse and paralysis of neu
 A:Reference number: A49069; MUID:94006554; PMID:8402808
 A:Session: A49069
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-772 <LUO>
 A:Cross-references: GB:U02528; NID:9410078; PIDN:AAC59638.1; PID:9410079
 C:Superfamily: semaphorin

Query Match 17.5%; Score 632.5; DB 2; Length 772;
 Best Local Similarity 28.4%; Pred. No. 3.3e-40;
 Matches 195; Conservative 101; Mismatches 265; Indels 125; Gaps 28;

OY 29 LRILLMAAASQGLRSGRIFAVMKGVGDVND-----FGQTEPHTVLFHER 83
 DB 7 IALLSGVLLAGVNCQHNKNNPRLKLSYKEMESNNVTFPGLANGSSYHTFLDEE- 65
 OY 84 SSSVWVGGRGVYLFDFPEGRKNASVTVNIGSTR-----GSKGSCD---DKRCE 127
 DB 66 RSRLVYGKDHIFSPDLVNIKDFQIVPVYSTRDECKMAGKDLK-ECANFIVLKA 115
 OY 128 NYITLLERSE-GLACGTNARHPSCMNLVNGVVLGEM-----RGYAPFSPDENS 170
 DB 116 NFKVLKTYNQTLLYACGTGAFHPC-----TYIEVGHREDNIFKLENSHPENGGRKSPYDKLLT 169
 OY 171 PESPDSNVLFEEDVYSTRKQEVNGKIPRRFRIGSELYT---SDTVMONPOFIKATVHQ-DQ 227
 DB 170 PYDKLLTSLVLDGSLYSGTAADFMGRDFAIFRTLGHHPIRTDQHSRWLNDPKFISAHLSIESDN 229
 OY 228 TIV-HODQAYDDKIYFFREDNPDKNPEAPLVNSRYAQLCRGDGESSLSVKNWFLAAMLUCSDA 286
 DB 230 HILPESDNPEDDKIYFFERNALIDGELSGKATHARIQICKNDPFGHRL-VNKKWTFLLARLICSP 288
 OY 287 AMUCSDAATN---KNFNRLQDVFL--PDPSGQMDTRVYGVF---SNPMWYSAVCVSLGIDKYF 338
 DB 289 ARLICSVPGNIDTHTDELQVFLMFKDP---KNPVYGVFTTSSNIFKSGAVCMYSMDVRYVF 344
 OY 339 LGDIDKVF-----RTSSLKGYHSLPNRPGKC-----LPDQOQIPIETFPVADRHREVAOR 382
 DB 345 MTDVRRVFLGPAVYAHGDPNRYQWVYOGGRVYPRPGTCKPSTFGGFDSTKDLDPDVITFAARSHPMYNP 404
 OY 383 RHEVAQRYEPMGP---LKTPLFHSKYHYQAVVHMAQSHGETFVLLTLTDRGTIHK 438
 DB 405 SHPMYNPVEPFIINSRIMIKTDV---DYQFTQIVDVRVDAEDGQ-YDVMEIGDVGIVLKVVSIPKFT 460
 OY 439 VVE-FGEDEHSFAFNIM-ETQPPRRAALQIOTMSLDAERKRLVYSSQWESQVPLDLCEVYGGGCHGL 496
 DB 461 VVSIPTRETHLEEVLEEMTVREPTVATISAMELSTKQOOLYIGSTAGVADQLPDLHRDDIIGKACABCC 520
 OY 497 GGGGCHGCLMSRDPYCGMDGRCISY--SSERSVYLOSINPAEPHKECPNPKDCK---APLQKVS-A 548
 DB 521 GKACABCCCLARDPYCAMDSSCSRYEPTAKRRTRQDIRNDPDLTHCSDDLHNDHNGHSPERIYGV 580

QY 549 ADLQKSLAPNSRRYVLSCEPMSRHATYSWR-----HKENVEOS-----CEGHOSPMC 596
148744
Db 581 LBEKIIITYGENSTPLEECGPKSORAIVYWFQKONDHKEIKVDDRMIRTEOG----- 634
QY 597 ILFIENLTAAQGYGHVCEAOGSSYFR 622
Db 635 -LLRSLQRRDSGIYFCHAVEHGFIO 659
RESULT 4
148744
semaphorin A - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: 148744
Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates
A:Reference number: 148744; MUID:95267431; PMID:7748561
A:Accession: 148744
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-748 <RES>
A:Cross-references: EMBL:X85990; NID:9854323; PIDN:CAAS9982.1; PID:9854324
C:Genetics:
A:Gene: sema
C:Superfamily: semaphorin
Query Match 17.4%; Score 628.5; DB 2; Length 748;
Best Local Similarity 31.5%; Pred. No. 6.5e-40;
Matches 181; Conservative 76; Mismatches 244; Indels 73; Gaps 21;
QY 125 DEENITLLERSE-GLACGNARHPSG-----WNLVNGTVPLG-----EMRGVAPESP 174
Db 112 ECKMNFVRLHAAYNHHTLLACRTGAFHPICALRMATAGTHASTGPEKLEDGKTPYDP 171
QY 175 DENSILVFEEDVYSTIRKOEYNGKIPRRRIERGESELYT-----SDVWMONPQFIKA-TIV 230
Db 172 RRRPSPVLVGEELYSVTADLMGCRDTTIFRSLQNSLSTEPHDSWMLNEPFVKYFWIP 231
QY 231 HODQAYDQKIYFFREDNPDKNPE-APLVNSRYAOLCRDQOGESSLSVSKWTFILKAML 289
Db 232 ESENEDDDKTYFFRESAIVEAAPAMGRMSVRYGQICRNDLGGQSL-VNKKTTFLKARL 290
QY 290 VCS--DAATNKPNRLODFLLPDPGQMDT-RVYGVSNP--WNYSAVCYVSLGDD 343
Db 291 VCSVPGVEGDTHFDLQDFELL--SSRDQTPPLLYAVESTSGVFGSAYCVYSMDVR 347
QY 344 KYF-----RTSLKGYHSSLPNRPGKC-----LPDQDPIPTETFOVADRHPEV 387
Db 348 RFLGLPLPKKEGPTHOWSYOGKRVPRPGKCPSTFGFSSTKDPEDVIOFGRNHPLM 407
QY 388 AGRVEPMGLKPLP--HSKYHYQKVAVHRQASHGETFHVLYLTDRGTIHKV--VBP 442
Db 408 YNPVLPMG--GRPLFQVAGYFTFOIADRVAAADGH-YDVLFGTGVTLKVLSVPR 464
QY 443 GGOEHSFANINIEIOFRRAAALQITMSLDAERKLYVSSQWMEVQVPLDCEVYGGCG 502
Db 465 GRPNSEGLLELOVEFSAITSMQISSKROOLVVASRAAVALALHRCATLALGACAE 524
QY 503 CLMSRDPYCGMOGRCSISY--SSERSVLOSINPAEPHKECPNPKDKAPLOKVSAPNS 560
Db 525 CCLARDPYCAMOGSACTRPROPTAKRRFRODTRNGDPTSLCSDSSHVLEKKVLGVS 584
QY 561 -RYVLSCEPMESRHATYSWRH-----KENVEOSCEGHOSPMCILFIENLTAAQ 606
Db 585 GSAFLECEBRSLQAHQWTFQFQAGAEAAHQVLAEEVERTARG-----LLRGLRRQ 636
QY 607 QYGHVCEAOGSSYFREAHQWOLLPEDGIMAEHL 640
Db 637 DSGVYLVCAVEQGFQPLRLRLVHLVLSAAQAEHL 670

RESULT 5
148747
semaphorin D - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: 148747
Puschel, A.W.; Adams, R.H.; Betz, H.
Neuron 14, 941-948, 1995
A:Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creat
A:Reference number: 148744; MUID:95267431; PMID:7748561
A:Accession: 148747
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-772 <RES>
A:Cross-references: EMBL:X85993; NID:9854329; PIDN:CAAS9985.1; PID:9854330
C:Genetics:
A:Gene: semd
C:Superfamily: semaphorin
Query Match 17.2%; Score 621; DB 2; Length 772;
Best Local Similarity 27.5%; Pred. No. 2.5e-39;
Matches 189; Conservative 110; Mismatches 283; Indels 106; Gaps 27;
QY 36 LMAAASAOGLHRSQ-----PRIFAVKGVHGDQVVD-----FGOTEPTHVLFEHPGSSS 86
Db 10 LFNGVLLTARANKNNVPRKLKSYKEMLENNVITFNGLANSSYHTFLDEE-RSR 68
QY 87 VVWGRGKYYLDFEPGKNASVFTVNIQSTK-----GSCIDKRDCEVITLLERSE- 138
Db 69 LVYGAQDIHSEFVLNVIKDFQITVMPVSYTRDECKWACKDILK-ECANFIKYLEAYNOT 127
QY 139 GLACGTNARHSCMNLVNGTVPLGEM-----RGYAPSPDENSLVLF 182
Db 128 HLYACGTGAHPKPC-----TYLEVGHHPEDNIFKLQDSHFENGKRSKSPDPLLAASL 181
QY 183 EGDVEYSTIRKOEYNGKIPRRRIERGESELYT-----SDVWMONPQFIKATV-HODQAYDD 238
Db 182 IDCELYSGTAADPMGADPAIFRLGDHNPTRTQOHNSRLNDRFTLSAHLIPESDPEDD 241
QY 239 KIYFFREDNPDKNPEAPLVNSRYAOLCRDQOGESSLSVSKWTFILKAMLYSDAATN- 297
Db 242 KYFFERENALIGEHSGKATHAIGQICKNDEGHRSL-VNKKTTFLKARLCSVGPNG 300
QY 298 --KNEKRLQDFLL--PDPSGQMDTRVYGVF--SNPNYSAVCYVSLGDDIKF----- 346
Db 301 IDTHFEDLDVFLMNSKDP--KNPIYVGVTFTSSNIFKGSVAVCMYSMSDVARVFLGPY 356
QY 347 -----RTSLKGYHSSLPNRPGKC-----LPDQDPIPTETFOVADRHPEVAPQVEPM 394
Db 357 AHRDGNVQWVRYQGRVPRPTGCTSPKTFGGFDSTKDLDPDVITGRSHRPNVNFPI 416
QY 395 G-----PLKTRPLFHSKYHYQKVAVHRQASHGETFHVLYLTDRGTIHKV--PGEQHSF 449
Db 417 NNRPIMKITDV--NYQFOIIVDRVDAEDQ-YDVMFGLTGVTLKVLSVPRKETWMDL 472
QY 450 AFNIM-EIOPFRRAAALQITMSLDAERKLYVSSQWMEVQVPLDCEVYGGCGCLMSRD 508
Db 473 EYVLEEMTVFRRPTTISAMELSTKQOOLYIGTAGVADPLRHKICYGACAECCCLARD 532
QY 509 PYCGMOGRCSISY--SSERSVLOSINPAEPHKECPN-----PKDKAPLOKVSIA 557
Db 533 PYCAMOGSSCSRFPAPKRRTRKODLRNDPRLHCGDLDHDHNNHPSLEERTIYVE-- 590
QY 558 PMSRYVLSCEPMESRHATYSWRHKEENVEOSCEGHOSPMCILFIENLTAAQGYGHV 612
Db 591 -NSSTFLCSPKSQRALVYWFQFRRNRRSKREITRMGDHIIIRTEOGILLRSLQKDGSGNYL 649
QY 613 CEAOEGSYFREAHQWOLLPEDGIMAEHL 640
Db 650 CHAVEHGFQOTLLKVTLL--EVIDTEHL 674


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Best Local Similarity 20.00; Pred. NO. 1.36-37;
Matches 175; Conservative 96; Mismatches 265; Indels 71; Gaps 23

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Matches 175; Conservative 96; Mismatches 265; Indels 71; Gaps 23


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Db 57 LLAADG-DSLVLGARNAYV-----NLSTLSVNHKIDMKPRAEHIECIMGK--S 105
Oy 123 KRDCENYITLLERSEGL-LACGTNARHPSCWNLVNGTVPLG-----EMRGYAPSP 174
Db 106 KTDCCNRYRLARKKASVGLVCGTHAFSPKREY---YTERGINTROFDQGISPYDP 162
Oy 175 DENSLVL-----FEGDE--VY-----STIRKOEYNGKIPRRR 204
Db 163 KHNSSALVYPTGNQLFVATVTDVFGNDALYRKTIDEFPPSSKANIRQSYDAR----- 217
Oy 205 RIRGSELYSTVWQNPQFIATVHODQATDKIYFFRE--DNPRKNPAPLAVSKY 262
Db 218 -----VLNAPNFV-ATF-----AYKEHVYEFMERIASAIDNNEPDIYARV 258
Oy 263 AOLCDGOGESSLSVSKNFFLKALMYCS--DAATNKNFNRLQDVFLLPDSGQWRDR 320
Db 259 ARVCNDKDGARFAN-ERWTSYLKARLNCSLPSSGSPFFENLKAV---SDPIDAGNNH 314
Oy 321 -VYGVFNP---WNSAVCVYSLGIDIKVFRTSLKGYHSS-----LPNPRPGK 365
Db 315 VYVYFSTPDSQVRRMSAVCKEFMKKIRREFDNGTFKHONNAQSMMAFNREVPKPRPS 374
Oy 366 CLPDQQPIPTETFOYADHREVAQORVERPMGRLKTLFHSKYH-----YQKVAVHRMQASHG 421
Db 375 CSPDSTKLRENTVSTILHPLLR--PLPSVADPLVAGADRADLTQTLVLRVRAVGG 431
Oy 422 ETFHVLVLTTRGTLHKVYEPGEQESHFAFNIMEIQPFRRAAIQTMSLDAERRKLYSS 481
Db 432 HNYDLFTGTSDGKVLKVEVDGN---ATYQSATVFQGRPI--VNLTLTKESVIVS 485
Oy 482 QWEVSQVPLDCEVYGGCGHCLMSRDYCGMDQ--GRCI 519
Db 486 ADELASLEPVHNC-AQOTSCSKCVOLQDPHCAMDSSIARCV 524

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RESULT 15

JC5928

semaphorin F precursor - human

C:Species: Homo sapiens (man)

C:Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Nov-2000

C:Accession: JC5928

R:Simmons, A.D.; Puschel, A.W.; McPherson, J.D.; Overhauser, J.; Lovett, M.

Biochem. Biophys. Res. Commun. 242: 685-691, 1998

A:Title: Molecular cloning and mapping of human semaphorin F from the Cri-du-chat candid

A:Reference number: JC5928; MUID:98125554; PMID:9464278

A:Accession: JC5928

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-1074 <SIM>

A:Cross-references: GB:U52840; NID:g2772583; PIDN:AAC09473.1; PID:g2772584

A:Experimental source: Brain

A:Comment: This protein disrupts normal brain development and leads to some of the featu

C:Genetics:

A:Gene: semaF

C:Superfamily: human semaphorin F; thrombospondin type 1 repeat homology

F:1-20/Domain: signal sequence #status predicted <SIG>

F:50-53/Domain: semaphorin #status predicted <SEM>

F:840-896/Domain: thrombospondin type 1 repeat homology <THR3>

F:971-993/Domain: transmembrane #status predicted <TM>

Query Match 11.3%; Score 409; DB 2; Length 1074;

Best Local Similarity 29.5%; Pred. No. 7e-23;

Matches 147; Conservative 76; Mismatches 206; Indels 70; Gaps 28;

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Oy 64 ODRVDFGQTEPHTVLFHHPGSSVWVGKGYLLDFPEGKNASVRYVN---IGSTKSG 120
Db 53 KNAADFQ-----LTFPGQKELVVGARN--YLRLQLEDLSLQAVWECEDEATKAC 104
Oy 121 L-----DKRDCENYITLLERSEGLACGTNARHPSCWNLVNGTVPL--GEMRGYA--PFS 173
Db 105 YSKGSKRECCQNYITVLLVGGRLFTCGTNAFTPVCTNRSLSNLAEIHQISGMARCPYS 164

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Oy 174 PDENSLVLF-EGDEVYSTIRKOEYNGKIPRRIRG-----ESELYSQTVWQNPQFIKA 227
Db 165 POHNSTALLTAGCELYAA--TAMDFGDRDAIYRSGLIPRLTAQYNSKW--LNEBNFV-- 220
Oy 228 TIVHODQAVD--DKIYFPRDNPPKNPAPLAVSRVADLCGDDGOGESSLSVSKNFFL 285
Db 221 -----SSYDIGNFTYFFERE--NAVEHDCGKTVFSRAARVCNNDIGRFLLE-DTMTTFM 272
Oy 286 KALMYCS--DAATNKNFNRLQDVFLLPDSGQWRDRYVGVFSNPNV---YSAVCVYSLGD 341
Db 273 KARLNCSTRGEVPTFYNELQSTFFLELD-----LIYIFTTNNNSIASAVCFNLSA 326
Oy 342 IDKVFRTSSLKGYHSS-----LPNPRG-KCLPDQQPIPTETFOYADHREVAQORV--- 391
Db 327 IQAOF--SGPFKYQENSAMLPYPNPNPHQCGTVDOGL---YVNLTERNLQDAOKFITY 382
Oy 392 -EPMGRLKLT-PLF-HSKYHQAQVAVHRMQASHGEFHVLYLTDRGTTHKVEP--GEQH 447
Db 383 HEVQPVTVTPSFMEDNSRFSHVAADVQVQGREA-LVHIYLTADYGTLLKKVAPLNLQSS 441
Oy 448 SFAFNIMEIQPFRRAAIQTMSLDAERRKLYSSQWEVSQVPLDCEVYGGCGHCLMSR 507
Db 442 SCLLEIEILFPRRRRPIRSLQILHSQSVLFVGLREHVYKIPKRCQFYRTR-STCIGAQ 500
Oy 508 DRYCGMD--QGRCTIYSS 524
Db 501 DRYCGMDVVMKKCTSLSEES 519

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Search completed: March 14, 2003, 09:27:40

Job time : 24.4774 secs